SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: EVANS, RONALD M.
               MCKEOWN, MICHAEL B.
               ORO, ANTHONY E.
               SEGRAVES, WILLIAM A.
               YAO, TSO-PANG

    (ii) TITLE OF INVENTION: MULTIMERIC FORMS OF MEMBERS OF THE
        STEROID/THYROID SUPERFAMILY OF RECEPTORS WITH THE
        ULTRASPIRACLE RECEPTOR

    (iii) NUMBER OF SEQUENCES: 29

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
        (B) STREET: 444 South Flower Street, Suite 2000
        (C) CITY: Los Angeles
        (D) STATE: California
        (E) COUNTRY: United States
        (F) ZIP: 90071

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 07/907,908
        (B) FILING DATE: 02-JUL-1992
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Reiter,, Stephen E.
        (B) REGISTRATION NUMBER: 31192
        (C) REFERENCE/DOCKET NUMBER: P41 9321

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (619) 546-4737
        (B) TELEFAX: (619) 546-9392

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2304 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 163..1701

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGACACGGTG GCGTTGGCAA AGTGAAACCC CAACAGAGAG GCGAAAGCGA GCCAAGACAC      60

ACCACATACA CACGAAGAGA ACGAGCAAGA AGAAACCGGT AGGCGGAGGA GGCGCTGCCC     120
```

```
CCAGTTCCTC CAATATACCC AGCACCACAT CACAAGCCCA GG ATG GAC AAC TGC          174
                                              Met Asp Asn Cys
                                                1

GAC CAG GAC GCC AGC TTT CGG CTG AGC CAC ATC AAG GAG GAG GTC AAG          222
Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys Glu Glu Val Lys
 5                   10                  15                  20

CCG GAC ATC TCG CAG CTG AAC GAC AGC AAC AAC AGC AGG TTT TCG CCC          270
Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser Ser Phe Ser Pro
                 25                  30                  35

AAG GCC GAG AGT CCC GTG CCC TTC ATG CAG GCC ATG TCC ATG GTC CAC          318
Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met Ser Met Val His
                 40                  45                  50

GTG CTG CCC GGC TCC AAC TCC GCC AGC TCC AAC AAC AAC AGC GCT GGA          366
Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn Asn Ser Ala Gly
             55                  60                  65

GAT GCC CAA ATG GCG CAG GCG CCC AAT TCG GCT GGA GGC TCT GCC GCC          414
Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly Gly Ser Ala Ala
         70                  75                  80

GCT GCA GTC CAG CAG CAG TAT CCG CCT AAC CAT CCG CTG AGC GGC AGC          462
Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro Leu Ser Gly Ser
 85                  90                  95                  100

AAG CAC CTC TGC TCT ATT TGC GGG GAT CGG GCC AGT GGC AAG CAC TAC          510
Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr
                 105                 110                 115

GGC GTG TAC AGC TGT GAG GGC TGC AAG GGC TTC TTT AAA CGC ACA GTG          558
Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val
                 120                 125                 130

CGC AAG GAT CTC ACA TAC GCT TGC AGG GAG AAC CGC AAC TGC ATC ATA          606
Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg Asn Cys Ile Ile
             135                 140                 145

GAC AAG CGG CAG AGG AAC CGC TGC CAG TAC TGC CGC TAC CAG AAG TGC          654
Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys
         150                 155                 160

CTA ACC TGC GGC ATG AAG CGC GAA GCG GTC CAG GAG GAG CGT CAA CGC          702
Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg
165                 170                 175                 180

GGC GCC CGC AAT GCG GCG GGT AGG CTC AGC GCC AGC GGA GGC GGC AGT          750
Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser Gly Gly Gly Ser
                 185                 190                 195

AGC GGT CCA GGT TCG GTA GGC GGA TCC AGC TCT CAA GGC GGA GGA GGA          798
Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln Gly Gly Gly Gly
                 200                 205                 210

GGA GGC GGC GTT TCT GGC GGA ATG GGC AGC GGC AAC GGT TCT GAT GAC          846
Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn Gly Ser Asp Asp
                 215                 220                 225

TTC ATG ACC AAT AGC GTG TCC AGG GAT TTC TCG ATC GAG CGC ATC ATA          894
Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile Glu Arg Ile Ile
         230                 235                 240

GAG GCC GAG CAG CGA GCG GAG ACC CAA TGC GGC GAT CGT GCA CTG ACG          942
Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp Arg Ala Leu Thr
245                 250                 255                 260
```

```
TTC CTG CGC GTT GGT CCC TAT TCC ACA GTC CAG CCG GAC TAC AAG GGT        990
Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro Asp Tyr Lys Gly
                265                 270                 275

GCC GTG TCG GCC CTG TGC CAA GTG GTC AAC AAA CAG CTC TTC CAG ATG       1038
Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln Leu Phe Gln Met
            280                 285                 290

GTC GAA TAC GCG CGC ATG ATG CCG CAC TTT GCC CAG GTG CCG CTG GAC       1086
Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln Val Pro Leu Asp
            295                 300                 305

GAC CAG GTG ATT CTG CTG AAA GCC GCT TGG ATC GAG CTG CTC ATT GCG       1134
Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu Leu Leu Ile Ala
        310                 315                 320

AAC GTG GCC TGG TGC AGC ATC GTT TCG CTG GAT GAC GGC GGT GCC GGC       1182
Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp Gly Gly Ala Gly
325                 330                 335                 340

GGC GGG GGC GGT GGA CTA GGC CAC GAT GGC TCC TTT GAG CGA CGA TCA       1230
Gly Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe Glu Arg Arg Ser
            345                 350                 355

CCG GGC CTT CAG CCC CAG CAG CTG TTC CTC AAC CAG AGC TTC TCG TAC       1278
Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln Ser Phe Ser Tyr
            360                 365                 370

CAT CGC AAC AGT GCG ATC AAA GCC GGT GTG TCA GCC ATC TTC GAC CGC       1326
His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala Ile Phe Asp Arg
            375                 380                 385

ATA TTG TCG GAG CTG AGT GTA AAG ATG AAG CGG CTG AAT CTC GAC CGA       1374
Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu Asn Leu Asp Arg
            390                 395                 400

CGC GAG CTG TCC TGC TTG AAG GCC ATC ATA CTG TAC AAC CCG GAC ATA       1422
Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr Asn Pro Asp Ile
405                 410                 415                 420

CGC GGG ATC AAG AGC CGG GCG GAG ATC GAG ATG TGC CGC GAG AAG GTG       1470
Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys Arg Glu Lys Val
            425                 430                 435

TAC GCT TGC CTG GAC GAG CAC TGC CGC CTG GAA CAT CCG GGC GAC GAT       1518
Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His Pro Gly Asp Asp
            440                 445                 450

GGA CGC TTT GCG CAA CTG CTG CTG CGT CTG CGC CGC TTT GCG ATC GAT       1566
Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Arg Arg Phe Ala Ile Asp
            455                 460                 465

CAG CCT GAA GTG CCA GGA TCA CCT GTT CCT CTT CCG CAT TAC CAG CGA       1614
Gln Pro Glu Val Pro Gly Ser Pro Val Pro Leu Pro His Tyr Gln Arg
        470                 475                 480

CCG GCC GCT GGA GGA GCT CTT TCT CGA GCA GCT GGA GGC GCC GCC GCC       1662
Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly Gly Ala Ala Ala
485                 490                 495                 500

ACC CGG CCT GGC GAT GAA ACT GGA GTA GGG TCC CGA CTC TAAAGTCGCC       1711
Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg Leu
            505                 510

CCCGTTCTCC ATCCGAAAAA TGTTTCATTG TGATTGCGTT TGTTTGCATT TCTCCTCTCT   1771

\ATCCCTACAA AAGCCCCCTA ATATTACGCA AAATGTGTAT GTAATTGTTT ATTTTTTTTT   1831
```

TATTACCTAA TATTATTATT ATTATTGATA TAGAAAATGT TTTCCTTAAG ATGAAGATTA   1891

GCCTCCTCGA CGTTTATGTC CCAGTAAACG AAAAACAAAC AAAATCCAAA ACTTGAAAAG   1951

AACACAAAAC ACGAACGAGA AAATGCACAC AAGCAAAGTA AAAGTAAAAG TTAAACTAAA   2011

GCTAAACGAG TAAAGATATT AAAATAACGG TTAAAATTAA TGCATAGTTA TGATCTACAG   2071

ACGTATGTAA ACATACAAAT TCAGCATAAA TATATATGTC AGCAGGGGCA TATCTGCGGT   2131

GCTGGCCCCG TTCTAAACCA ATTGTAATTA CTTTTTAACA TAAATTTACC CAAAACGTTA   2191

TCAATTAGAT GCGAGATACA AAAATCACCG ACGAAACCA ACAAAATATA TCTATGTATA   2251

AAAAATATAA GCTGCATAAC AAAAAAAAAA AAAAAAAAAA AAAAAAAAA AAA   2304

(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 513 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Asp Asn Cys Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys
 1               5                  10                  15

Glu Glu Val Lys Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser
            20                  25                  30

Ser Phe Ser Pro Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met
        35                  40                  45

Ser Met Val His Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn
    50                  55                  60

Asn Ser Ala Gly Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly
65                  70                  75                  80

Gly Ser Ala Ala Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro
                85                  90                  95

Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser
            100                 105                 110

Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe
        115                 120                 125

Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg
    130                 135                 140

Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg
145                 150                 155                 160

Tyr Gln Lys Cys Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu
                165                 170                 175

Glu Arg Gln Arg Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser
            180                 185                 190

Gly Gly Gly Ser Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln
        195                 200                 205
```

Gly Gly Gly Gly Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn
    210   215   220

Gly Ser Asp Asp Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile
225   230   235   240

Glu Arg Ile Ile Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp
        245   250   255

Arg Ala Leu Thr Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro
        260   265   270

Asp Tyr Lys Gly Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln
        275   280   285

Leu Phe Gln Met Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln
        290   295   300

Val Pro Leu Asp Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu
305   310   315   320

Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp
        325   330   335

Gly Gly Ala Gly Gly Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe
        340   345   350

Glu Arg Arg Ser Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln
        355   360   365

Ser Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala
        370   375   380

Ile Phe Asp Arg Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu
385   390   395   400

Asn Leu Asp Arg Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr
        405   410   415

Asn Pro Asp Ile Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys
        420   425   430

Arg Glu Lys Val Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His
        435   440   445

Pro Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Arg Arg
        450   455   460

Phe Ala Ile Asp Gln Pro Glu Val Pro Gly Ser Pro Val Pro Leu Pro
465   470   475   480

His Tyr Gln Arg Pro Ala Ala Gly Gly Ala Leu Ser Arg Ala Ala Gly
          485   490   495

Gly Ala Ala Ala Thr Arg Pro Gly Asp Glu Thr Gly Val Gly Ser Arg
        500   505   510

Leu

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 71 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: unknown
        (D) TOPOLOGY: unknown

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Cys Xaa Xaa Cys Xaa Xaa Asp Xaa Ala Xaa Gly Xaa Tyr Xaa Xaa Xaa
1               5                   10              15

Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa
            20                  25              30

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
        35                  40                  45

Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa
    50                  55                  60

Lys Cys Xaa Xaa Xaa Gly Met
65                  70
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGTCAAGGA GGTCA   15

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGTGAATGA GGACA   15

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTGAACGG GGGCA   15

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 15 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCACGAG GTTCA   15

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGTCACAGG AGGTCA   16

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGTGACAGG AGGTCA   16

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGGTGACAGG AGGACA   16

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGTTAGGGG AGGACA   16

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 16 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGTCATTTC AGGTCC   16

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGTCACCAG GAGGTCA   17

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGGTGAACAG GAGGTCA   17

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTTCACCGA AAGTTCA   17

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTTCACCGA AAGTTCA   17

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTCACTGA CAGGGCA   17

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 17 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGTCATTCA GAGTTCA   17

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 34 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAGCTTAAGG GTTCACCGAA AGTTCACTCA GCTT   34

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 38 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAGCTTAAGG GTTCACCGAA AGTTCACTCG CATAGCTT   38

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 43 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGCTTAAGG GTTCACCGAA AGTTCACTCG CATATATTAG CTT   43

(2) INFORMATION FOR SEQ ID NO:22:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 62 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCTCGATGG ACAAGTGCAT TGAACCCTTG AGCTACCTGT TCACGTAACT TGGGAACTTC   60

GA   62

(2) INFORMATION FOR SEQ ID NO:23:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 33 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCTGCGCCAC GGCGGCCGCC GGAGCTGTGC CTG   33

(2) INFORMATION FOR SEQ ID NO:24:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 29 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTGGGTATGC GCCTCGAGTG CGTCGTCCC   29

(2) INFORMATION FOR SEQ ID NO:25:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 13 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGGACAAAGG TCA   13

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATTGGACAAG TGCATTGAAC CCTTGTCTCT   30

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCTGTGCA TTGAACGTGC TCGA   24

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGAAGTGCA TTGAACCCGC TCGA   24

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAAAGGATCT TGACCCCAAT GAACTTCTTA   30